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RAW SEQUENCE LISTING PATENT APPLICATION US/09/422,999

DATE: 11/09/1999
TIME: 16:44:43

Input Set: I422999.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1  <110> APPLICANT: Kawasaki, Hiroaki
2      Graybiel, Ann
3      Housman, David
4  <120> TITLE OF INVENTION: Genes Integrating Signal Transduction Pathways
5  <130> FILE REFERENCE: MIT-103
6  <140> CURRENT APPLICATION NUMBER: US/09/422,999
7  <141> CURRENT FILING DATE: 1999-10-22
8  <150> EARLIER APPLICATION NUMBER: US 60/105,507
9  <151> EARLIER FILING DATE: 1998-10-23
10 <150> EARLIER APPLICATION NUMBER: US 60/108,685
11 <151> EARLIER FILING DATE: 1998-11-16
12 <160> NUMBER OF SEQ ID NOS: 18
13 <170> SOFTWARE: PatentIn Ver. 2.0
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15 <211> LENGTH: 2250
16 <212> TYPE: DNA
17 <213> ORGANISM: Mus musculus
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (166)..(1989)
21 <223> OTHER INFORMATION: CalDAG-GEFI
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25      gctctgagag tgtaacttgg gtctagccca ctggcaccgg cagcc atg gcg agc act 177
26                                     Met Ala Ser Thr
27                                     1
28      ctg gac ctg gac aag ggt tgc acc gtg gag gag ctg ctc cgt ggc tgt 225
29      Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu Leu Arg Gly Cys
30      5 10 15 20
31      atc gaa gcc ttt gat gac tct gga aag gtg cga gat cca cag cta gtg 273
32      Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val
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34      cgc atg ttt ctc atg atg cac ccc tgg tac ata cct tcc tct cag ctg 321
35      Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu
36      40 45 50
37      gct tcg aaa ctg ctc cac ttc tat cag caa tcc cgg aag gac aac tcc 369
38      Ala Ser Lys Leu Leu His Phe Tyr Gln Gln Ser Arg Lys Asp Asn Ser
39      55 60 65
40      aat tcc cta cag gtg aaa acc tgt cac ctg gtc agg tac tgg gtc tca 417
41      Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg Tyr Trp Val Ser
42      70 75 80
43      gcc ttc cca gca gag ttc gac ttg aac cca gag ctg gct gaa ccg atc 465
44      Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu Ala Glu Pro Ile

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49	agc ctc atc gac atc gag agt gtc ccc acc tac aag tgg aag cgg cag				561
50	Ser Leu Ile Asp Ile Glu Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln				
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52	gtg acc cag cgg aac cct gtg gaa cag aaa aag cgc aag atg tcc ctg				609
53	Val Thr Gln Arg Asn Pro Val Glu Gln Lys Lys Arg Lys Met Ser Leu				
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55	ttg ttt gat cac ttg gag cct atg gaa ctg gca gaa cat ctc acc tac				657
56	Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr				
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58	ttg gag tat cgg tcc ttc tgc aag atc ctg ttc cag gac tat cac agc				705
59	Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser				
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61	ttt gtg act cat ggc tgc act gta gac aat ccg gtc ctg gag cga ttc				753
62	Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe				
63		185	190	195	
64	atc tcc ctc ttc aac agt gtc tct cag tgg gtc caa ctc atg atc ctc				801
65	Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu				
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67	agc aag ccc aca gcc acg cag cgg gcg ctg gtc atc aca cat ttc gtg				849
68	Ser Lys Pro Thr Ala Thr Gln Arg Ala Leu Val Ile Thr His Phe Val				
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71	His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met				
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74	Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser Arg Leu Lys Glu				
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76	acc cac agc cat gtc agc cct gac acc atc aag ctc tgg gaa ggt ctg				993
77	Thr His Ser His Val Ser Pro Asp Thr Ile Lys Leu Trp Glu Gly Leu				
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79	aca gaa cta gtg aca gct act ggc aac tac agc aac tac cgg cga agg				1041
80	Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Ser Asn Tyr Arg Arg Arg				
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83	Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu Gly Val His Leu				
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85	aag gat cta gtg gct ctg cag ctg gct ctg cct gac tgg ctg gac cca				1137
86	Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp Trp Leu Asp Pro				
87		310	315	320	
88	ggt cgg acc cgg ctc aat gga gcc aag atg agg cag ctt ttc agc att				1185
89	Gly Arg Thr Arg Leu Asn Gly Ala Lys Met Arg Gln Leu Phe Ser Ile				
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91	ctg gag gag ttg gct atg gtg acc agt ctt cga cca cca gtg caa gcc				1233
92	Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro Pro Val Gln Ala				
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94	aac ccc gac ctg ctg agt ctg ctc acg gtg tcc ctg gac cag tat cag				1281

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98	Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg Glu Pro Arg Ser	
99	375 380 385	
100	aag tca tcg ccc acc agc ccc acc agc tgc acc ccg cct ccc cgg ccg	1377
101	Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro Pro Pro Arg Pro	
102	390 395 400	
103	cct gtg ctg gaa gag tgg acc tca gtt gcc aag cct aag ctg gac caa	1425
104	Pro Val Leu Glu Glu Trp Thr Ser Val Ala Lys Pro Lys Leu Asp Gln	
105	405 410 415 420	
106	gcc ttg gtg gcc gag cac att gag aag atg gtg gag tct gtg ttc cgg	1473
107	Ala Leu Val Ala Glu His Ile Glu Lys Met Val Glu Ser Val Phe Arg	
108	425 430 435	
109	aac ttt gac gtt gat ggg gac ggt cac atc tcc cag gag gag ttc cag	1521
110	Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln Glu Glu Phe Gln	
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112	atc atc cgg ggc aac ttc cct tat ctc agc gcc ttt ggg gac ttg gac	1569
113	Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe Gly Asp Leu Asp	
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115	cag aac cag gat ggc tgc atc agc cgg gag gag atg att tcc tac ttc	1617
116	Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met Ile Ser Tyr Phe	
117	470 475 480	
118	ctg cgc tcc agc tcc gtg ctg gga ggc cgc atg ggc ttc gta cac aac	1665
119	Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly Phe Val His Asn	
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121	ttc cag gag agt aac tcg cta agg ccg gtc gcc tgc cga cac tgc aaa	1713
122	Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys Arg His Cys Lys	
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124	gct ctg atc ctg ggc atc tac aag cag ggc ctc aaa tgt aga gct tgt	1761
125	Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg Ala Cys	
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128	Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu Ser Val Glu Cys	
129	535 540 545	
130	cgc cgc cgc gcc cag agt gtg agc ctg gag ggc tct gca ccc tct ccc	1857
131	Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser Ala Pro Ser Pro	
132	550 555 560	
133	tca ccc aca cat acc cac cat cgg gcc ttc agc ttc tcc ctg cct cgc	1905
134	Ser Pro Thr His Thr His His Arg Ala Phe Ser Phe Ser Leu Pro Arg	
135	565 570 575 580	
136	cca ggc agg cgc agc tct cgg cct cca gag atc cgt gaa gag gag gtg	1953
137	Pro Gly Arg Arg Ser Ser Arg Pro Pro Glu Ile Arg Glu Glu Glu Val	
138	585 590 595	
139	cag act gtg gaa gat ggt gtg ttc gac atc cac tta taagacgtg	1999
140	Gln Thr Val Glu Asp Gly Val Phe Asp Ile His Leu	
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142	tgactatcaa ggactcattc ctgccttgga gaaaagactt ggagcagagc agggagccag	2059
143	ggattctggg gcaggagggtt ggggctgaag gtgggggaag ttgaagggtg catgcactga	2119
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155      20          25          30
156      Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro
157      35          40          45
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162      Tyr Trp Val Ser Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu
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168      Trp Lys Arg Gln Val Thr Gln Arg Asn Pro Val Glu Gln Lys Lys Arg
169      130         135         140
170      Lys Met Ser Leu Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu
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172      His Leu Thr Tyr Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln
173      165         170         175
174      Asp Tyr His Ser Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val
175      180         185         190
176      Leu Glu Arg Phe Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln
177      195         200         205
178      Leu Met Ile Leu Ser Lys Pro Thr Ala Thr Gln Arg Ala Leu Val Ile
179      210         215         220
180      Thr His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe
181      225         230         235         240
182      Asn Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser
183      245         250         255
184      Arg Leu Lys Glu Thr His Ser His Val Ser Pro Asp Thr Ile Lys Leu
185      260         265         270
186      Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Ser Asn
187      275         280         285
188      Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu
189      290         295         300
190      Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp
191      305         310         315         320
192      Trp Leu Asp Pro Gly Arg Thr Arg Leu Asn Gly Ala Lys Met Arg Gln
193      325         330         335
194      Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro

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199          370          375          380
200  Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro
201  385          390          395          400
202  Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser Val Ala Lys Pro
203          405          410          415
204  Lys Leu Asp Gln Ala Leu Val Ala Glu His Ile Glu Lys Met Val Glu
205          420          425          430
206  Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln
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208  Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe
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211  465          470          475          480
212  Ile Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly
213          485          490          495
214  Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys
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216  Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys
217          515          520          525
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219          530          535          540
220  Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser
221  545          550          555          560
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223          565          570          575
224  Ser Leu Pro Arg Pro Gly Arg Arg Ser Ser Arg Pro Pro Glu Ile Arg
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239  ggagcgcagc ctgggcccag cccaccccgc gccggcggcc atg gca ggc acc ctg 175
240                                     Met Ala Gly Thr Leu
241                                     1 5
242  gac ctg gac aag ggc tgc acg gtg gag gag ctg ctc cgc ggg tgc atc 223
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VERIFICATION SUMMARY
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